

What is claimed is:

1. A method of determining a comparative expression profile in an individual, comprising:

(a) determining a multidimensional coordinate  
5 point representative of the expression levels of a sample of molecules in a population of molecules in a specimen from said individual;

(b) comparing said multidimensional coordinate point to a health-associated reference expression region of  
10 said sample of molecules; and

(c) determining if said multidimensional coordinate point is within or outside said health-associated reference expression region, wherein said multidimensional coordinate point within said health-associated reference  
15 expression region indicates a reference expression profile and wherein said multidimensional coordinate point outside said health-associated reference expression region indicates a perturbed expression profile.

2. The method of claim 1, further comprising the  
20 step of inputting the expression level of said molecules in said sample.

3. The method of claim 1, further comprising the step of determining the expression level of said molecules in said sample.

4. The method of claim 3, wherein the expression levels of said sample of molecules in said specimen are determined by direct comparison with reference expression levels correlated with health-associated reference  
5 expression intervals of said molecules in said sample.

5. The method of claim 3, further comprising the step of contacting said specimen with a target.

6. The method of claim 1, wherein said reference expression profile indicates a reference health state in  
10 said individual.

7. The method of claim 1, wherein said perturbed expression profile indicates a disease state in said individual.

8. The method of claim 1, wherein said perturbed  
15 expression profile indicates the course of a disease.

9. The method of claim 1, wherein said specimen is selected from the group consisting of leukocytes, blood, and serum.

10. The method of claim 5, wherein said target is  
20 an array.

11. The method of claim 1, wherein said molecules in said specimen comprise nucleic acids.

12. The method of claim 5, wherein said target comprises nucleic acid ligands.

13. The method of claim 1, wherein said molecules in said specimen comprise polypeptides.

14. The method of claim 5, wherein said target comprises antibody ligands.

5 15. The method of claim 1, wherein said molecules in said specimen comprise small molecules.

16. The method of claim 1, further comprising the step of reporting whether a reference expression profile or a perturbed expression profile is indicated.

10 17. A method of determining a comparative expression profile in an individual, comprising comparing the expression levels of a sample of molecules in a population of molecules in a specimen from said individual with health-associated reference expression intervals of  
15 said sample of molecules, wherein expression levels within said health-associated reference expression intervals indicate a reference expression profile and wherein expression levels outside said health-associated reference expression intervals indicate a perturbed expression  
20 profile.

18. The method of claim 17, further comprising the step of inputting the expression level of said molecules in said sample.

19. The method of claim 17, further comprising the step of determining the expression level of said molecules in said sample.

20. The method of claim 19, wherein the  
5 expression levels of said sample of molecules in said specimen are determined by direct comparison with reference expression levels correlated with health-associated reference expression intervals of said molecules in said sample.

10 21. The method of claim 19, further comprising the step of contacting said specimen with a target.

22. The method of claim 17, wherein said reference expression profile indicates a reference health state in said individual.

15 23. The method of claim 17, wherein said perturbed expression profile indicates a disease state in said individual.

24. The method of claim 17, wherein said  
20 perturbed expression profile indicates the course of a disease.

25. The method of claim 17, wherein said specimen is selected from the group consisting of leukocytes, blood, and serum.

26. The method of claim 17, wherein said target  
25 is an array.

27. The method of claim 17, wherein said molecules in said specimen comprise nucleic acids.

28. The method of claim 21, wherein said target comprises nucleic acid ligands.

5 29. The method of claim 17, wherein said molecules in said specimen comprise polypeptides.

30. The method of claim 21, wherein said target comprises antibody ligands.

10 31. The method of claim 17, wherein said molecules in said specimen comprise small molecules.

32. The method of claim 17, further comprising the step of reporting whether a reference expression profile or a perturbed expression profile is indicated.

15 33. A method of determining a comparative expression profile in an individual, comprising:

(a) comparing the expression level of a molecule in a specimen from said individual with a health-associated reference expression interval of said molecule; and

20 (b) assigning a value of 0 if said expression level is within said health-associated reference expression interval, assigning a positive numerical value if said expression level is greater than said health-associated reference expression interval, or assigning a negative numerical value if said expression level is less than said

health-associated reference expression interval, wherein  
said expression level within said health-associated  
reference expression interval indicates a reference  
expression profile and wherein said expression level outside  
5 said health-associated reference expression interval  
indicates a perturbed expression profile.

34. The method of claim 33, wherein steps (a) and  
(b) are repeated one or more times.

35. The method of claim 33, further comprising  
10 the step of reporting whether a reference expression profile  
or a perturbed expression profile is indicated.

36. The method of claim 34, wherein a value of 0  
for all molecules assigned a value indicates a reference  
expression profile in said individual.

15 37. The method of claim 34, wherein said positive  
values are summed to generate a positive summation value.

38. The method of claim 37, wherein a positive  
summation value of 1 or greater indicates said individual  
has a perturbed expression profile.

20 39. The method of claim 38, wherein said  
perturbed expression profile indicates a disease state in  
said individual.

40. The method of claim 38, wherein said  
perturbed expression profile indicates the course of a  
25 disease.

41. The method of claim 34, wherein said negative values are summed to generate a negative summation value.

42. The method of claim 41, wherein a negative summation value of -1 or less indicates said individual has  
5 a perturbed expression profile.

43. The method of claim 42, wherein said perturbed expression profile indicates a disease state in said individual.

44. The method of claim 42, wherein said  
10 perturbed expression profile indicates the course of a disease.

45. The method of claim 34, wherein the absolute values of said positive and negative values are summed to generate a summation value.

46. The method of claim 45, wherein a summation  
15 value of 1 or greater indicates said individual has a perturbed expression profile.

47. The method of claim 33, further comprising  
the step of inputting the expression level of said molecule  
20 in said specimen.

48. The method of claim 33, further comprising  
the step of determining the expression level of said  
molecule in said specimen.

49. The method of claim 48, wherein the expression levels of said sample of molecules in said specimen are determined by direct comparison with reference expression levels correlated with health-associated  
5 reference expression intervals of said molecules in said sample.

50. The method of claim 48, further comprising the step of contacting said specimen with a target.

51. The method of claim 33, wherein said specimen  
10 is selected from the group consisting of leukocytes, blood, and serum.

52. The method of claim 50, wherein said target is an array.

53. The method of claim 33, wherein said molecule  
15 in said specimen comprises nucleic acids.

54. The method of claim 50, wherein said target comprises nucleic acid ligands.

55. The method of claim 33, wherein said molecule in said specimen comprises polypeptides.

56. The method of claim 50, wherein said target  
20 comprises antibody ligands.

57. The method of claim 33, wherein said molecules in said specimen comprise small molecules.



58. A method of determining a comparative expression profile in an individual, comprising comparing the expression levels of a sample of molecules in a population of molecules in a specimen from said individual  
5 with reference expression levels correlated with health-associated reference expression intervals of said sample of molecules, wherein expression levels within said health-associated reference expression intervals indicate a reference expression profile and wherein expression levels  
10 outside said health-associated reference expression intervals indicate a perturbed expression profile.

59. The method of claim 58, further comprising the step of inputting the expression level of said molecules in said sample.

15 60. The method of claim 58, further comprising the step of determining the expression level of said molecules in said sample.

20 61. The method of claim 58, wherein said reference expression profile indicates a reference health state in said individual.

62. The method of claim 58, wherein said perturbed expression profile indicates a disease state in said individual.

25 63. The method of claim 58, wherein said perturbed expression profile indicates the course of a disease.

64. The method of claim 58, wherein said specimen is selected from the group consisting of leukocytes, blood and serum.

65. A method of diagnosing a disease, comprising:

5 (a) determining the expression levels of a sample of molecules in a population of molecules in a specimen from an individual;

10 (b) comparing said expression levels with a health-associated reference expression region of said sample of molecules; and

15 (c) determining if said expression levels of said sample of molecules is within or outside said health-associated reference expression region, wherein expression levels within said health-associated reference expression region indicates a reference health state and wherein expression levels outside said health-associated reference expression region indicates a disease state.

20 66. The method of claim 65, further comprising the step of inputting the expression level of said molecules in said sample.

67. The method of claim 65, further comprising the step of determining the expression level of said molecules in said sample.

68. The method of claim 67, wherein the expression levels of said sample of molecules in said specimen are determined by direct comparison with reference expression levels correlated with health-associated  
5 reference expression intervals of said molecules in said sample.

69. The method of claim 67, further comprising the step of contacting said specimen with a target.

70. The method of claim 65, wherein said  
10 reference expression profile indicates a reference health state in said individual.

71. The method of claim 65, wherein said perturbed expression profile indicates a disease state in said individual.

72. The method of claim 65, wherein said  
15 perturbed expression profile indicates the course of a disease.

73. The method of claim 65, wherein said specimen is selected from the group consisting of leukocytes, blood,  
20 and serum.

74. The method of claim 69, wherein said target is an array.

75. The method of claim 65, wherein said molecules in said specimen comprise nucleic acids.

76. The method of claim 69, wherein said target comprises nucleic acid ligands.

77. The method of claim 65, wherein said molecules in said specimen comprise polypeptides.

5 78. The method of claim 69, wherein said target comprises antibody ligands.

79. The method of claim 65, wherein said molecules in said specimen comprise small molecules.

80. The method of claim 65, further comprising  
10 the step of reporting whether a reference expression profile or a perturbed expression profile is indicated.

81. A method of diagnosing a disease, comprising:

(a) contacting a specimen with a target;

(b) determining the expression levels of a sample  
15 of molecules in a population of molecules in said specimen;  
and

(c) comparing said expression levels with a health-associated reference expression interval of said sample of molecules, wherein expression levels within said  
20 health-associated reference expression interval indicates a reference health state and wherein an expression level outside said health-associated reference expression interval indicates a disease state.

82. The method of claim 81, wherein said disease state is selected from the group consisting of diabetes and cancer.

83. The method of claim 81, wherein said specimen  
5 is selected from the group consisting of leukocytes, blood, and serum.

84. The method of claim 81, wherein said target is an array.

85. The method of claim 81, wherein said molecule  
10 in said specimen comprises nucleic acids.

86. The method of claim 81, wherein said target comprises nucleic acid ligands.

87. The method of claim 81, wherein said molecule in said specimen comprises polypeptides.

88. The method of claim 81, wherein said target  
15 comprises antibody ligands.

89. The method of claim 81, wherein said molecules in said specimen comprise small molecules.

90. A method of diagnosing a health state in an  
20 individual, comprising:

(a) determining the expression levels of a sample of molecules in a population of molecules in a specimen from an individual;

(b) comparing said expression levels with a health-associated reference expression region of said sample of molecules; and

(c) determining if said expression levels of said  
5 sample of molecules is within or outside said health-associated reference expression region, wherein expression levels within said health-associated reference expression region indicates a reference health state and wherein  
10 expression levels outside said health-associated reference expression region indicates a perturbed health state.

91. The method of claim 90, further comprising the step of inputting the expression level of said molecules in said sample.

92. The method of claim 90, further comprising  
15 the step of determining the expression level of said molecules in said sample.

93. The method of claim 92, wherein the expression levels of said sample of molecules in said specimen are determined by direct comparison with reference  
20 expression levels correlated with health-associated reference expression intervals of said molecules in said sample.

94. The method of claim 92, further comprising the step of contacting said specimen with a target.

95. The method of claim 90, wherein said perturbed health state indicates a disease state in said individual.

96. The method of claim 90, wherein said  
5 perturbed expression profile indicates the course of a disease.

97. The method of claim 90, wherein said specimen is selected from the group consisting of leukocytes, blood, and serum.

10 98. The method of claim 94, wherein said target is an array.

99. The method of claim 90, wherein said molecules in said specimen comprise nucleic acids.

100. The method of claim 94, wherein said target  
15 comprises nucleic acid ligands.

101. The method of claim 90, wherein said molecules in said specimen comprise polypeptides.

102. The method of claim 94, wherein said target comprises antibody ligands.

20 103. The method of claim 90, wherein said molecules in said specimen comprise small molecules.

104. The method of claim 90, further comprising the step of reporting whether a reference expression profile or a perturbed expression profile is indicated.

105. A method of diagnosing a health state in an individual, comprising:

(a) comparing the expression level of a molecule in a specimen from said individual with a health-associated reference expression interval of said molecule; and

(b) assigning a value of 0 if said expression level is within said health-associated reference expression interval, assigning a positive numerical value if said expression level is greater than said health-associated reference expression interval, or assigning a negative numerical value if said expression level is less than said health-associated reference expression interval, wherein a value of 0 indicates a reference health state and wherein a positive or negative numerical value indicates a perturbed health state.

106. The method of claim 105, wherein steps (a) and (b) are repeated one or more times.

107. The method of claim 105, further comprising the step of reporting whether a reference health state or a perturbed health state is indicated.

108. The method of claim 105, wherein a value of 0 for all molecules assigned a value indicates a reference health state.



109. The method of claim 105, wherein said positive values are summed to generate a positive summation value.

110. The method of claim 109, wherein a positive  
5 summation value of 1 or greater indicates a perturbed health state.

111. The method of claim 110, wherein said perturbed health state indicates a disease state.

112. The method of claim 111, wherein said  
10 disease state is selected from the group consisting of diabetes and cancer.

113. The method of claim 111, wherein said perturbed expression profile indicates the course of a disease.

114. The method of claim 106, wherein said  
15 negative values are summed to generate a negative summation value.

115. The method of claim 114, wherein a negative  
20 summation value of -1 or less indicates a perturbed health state.

116. The method of claim 115, wherein said perturbed health state indicates a disease state.

117. The method of claim 116, wherein said disease state is selected from the group consisting of diabetes and cancer.

118. The method of claim 115, wherein said  
5 perturbed expression profile indicates the course of a disease.

119. The method of claim 106, wherein the absolute values of said positive and negative values are summed to generate a summation value.

120. The method of claim 106, wherein a summation  
10 value of 1 or greater indicates said individual has a perturbed health state.

121. The method of claim 120, wherein said perturbed health state indicates a disease state.

122. The method of claim 121, wherein said  
15 disease state is selected from the group consisting of diabetes and cancer.

123. The method of claim 120, wherein said  
20 perturbed expression profile indicates the course of a disease.

124. The method of claim 105, further comprising the step of inputting the expression level of said molecule in said specimen.

125. The method of claim 105, further comprising the step of determining the expression level of said molecule in said specimen.

5 126. The method of claim 125, wherein the expression levels of said sample of molecules in said specimen are determined by direct comparison with reference expression levels correlated with health-associated reference intervals of said molecules in said sample.

10 127. The method of claim 125, further comprising the step of contacting said specimen with a target.

128. The method of claim 105, wherein said specimen is selected from the group consisting of leukocytes, blood, and serum.

15 129. The method of claim 105, wherein said target is an array.

130. The method of claim 105, wherein said molecule in said specimen comprises nucleic acids.

131. The method of claim 127, wherein said target comprises nucleic acid ligands.

20 132. The method of claim 105, wherein said molecule in said specimen comprises polypeptides.

133. The method of claim 127, wherein said target comprises antibody ligands.

134. The method of claim 105, wherein said molecules in said specimen comprise small molecules.

135. A computer apparatus, comprising:

a processor;

5       main memory in communication with said processor;  
and

a comparative expression profiler in communication with said main memory configured to carrying out the computer-executed steps of:

10               (a) comparing the expression level of a molecule with a health-associated reference expression interval of said molecule; and

15               (b) assigning a value of 0 if said expression level is within said health-associated reference expression interval, assigning a positive numerical value if said expression level is greater than said health-associated reference expression interval, or assigning a negative numerical value if said expression level is less  
20       than said health-associated reference expression interval, wherein said expression level within said health-associated reference expression interval indicates a reference expression profile and wherein said expression level outside said  
25       health-associated reference expression interval indicates a perturbed expression profile.

136. The computer apparatus of claim 135, wherein steps (a) and (b) are repeated one or more times.

137. The computer apparatus of claim 135, wherein said comparative expression profiler further is configured  
5 to carry out the computer-executed step of determining said expression level of said molecule.

138. A computer apparatus, comprising:

a processor;

main memory in communication with said processor;

10 and

a comparative expression profiler in communication with said main memory configured to carrying out the computer-executed steps of:

15 (a) determining a multidimensional coordinate point representative of the expression levels of a sample of molecules from an individual; and

20 (b) comparing said multidimensional coordinate point with a health-associated reference expression region, wherein said multidimensional coordinate point within said health-associated reference expression region indicates a reference expression profile and wherein said multidimensional coordinate point  
25 outside said health-associated reference expression region indicates a perturbed expression profile.

139. The computer apparatus of claim 138, wherein said comparative expression profiler further is configured to carry out the computer-executed step of determining said expression level of said molecule.

5           140. A computer-readable medium having stored thereon a plurality of sequences of instructions, said plurality of sequences of instructions including sequences of instructions which, when executed by a processor, cause said processor to perform the steps of:

10           (a) comparing the expression level of a molecule with a health-associated reference expression interval of said molecule; and

             (b) assigning a value of 0 if said expression level is within said health-associated reference expression interval, assigning a positive numerical value if said expression level is greater than said health-associated reference expression interval, or assigning a negative numerical value if said expression level is less than said health-associated reference expression interval, wherein said expression level within said health-associated reference expression interval indicates a reference expression profile and wherein said expression level outside said health-associated reference expression interval indicates a perturbed expression profile.

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141. A computer-readable medium having stored thereon a plurality of sequences of instructions, said plurality of sequences of instructions including sequences of instructions which, when executed by a processor, cause  
5 said processor to perform the steps of:

(a) determining a multidimensional coordinate point representative of the expression levels of a sample of molecules from an individual; and

10 (b) comparing said multidimensional coordinate point with a health-associated reference expression region, wherein said multidimensional coordinate point within said health-associated reference expression region  
15 indicates a reference expression profile and wherein said multidimensional coordinate point outside said health-associated reference expression region indicates a perturbed expression profile.

142. A carrier wave carrying instructions for a processor, said instructions which, when executed by said processor, cause said processor to perform the steps of:

5 (a) comparing the expression level of a molecule with a health-associated reference expression interval of said molecule; and

10 (b) assigning a value of 0 if said expression level is within said health-associated reference expression interval, assigning a positive numerical value if said expression level is greater than said health-associated reference expression interval, or assigning a negative numerical value if said expression level is less than said health-associated reference expression interval, wherein said expression level within said health-associated reference expression interval indicates a reference expression profile and wherein said expression level outside said health-associated reference expression interval indicates a perturbed expression profile.

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143. A carrier wave carrying instructions for a processor, said instructions which, when executed by said processor, cause said processor to perform the steps of:

5 (a) determining a multidimensional coordinate point representative of the expression levels of a sample of molecules from an individual; and

10 (b) comparing said multidimensional coordinate point with a health-associated reference expression region, wherein said multidimensional coordinate point within said health-associated reference expression region indicates a reference expression profile and  
15 wherein said multidimensional coordinate point outside said health-associated reference expression region indicates a perturbed expression profile.